Attachment C

General Approach for Defining Within Population Structure:
Interior Columbia ESUs

Spatial structure varies greatly both within and among ESA defined chinook and steelhead populations. Both temporal and geographic variations exist within occupied systems, resulting in a wide array of spawning configurations. These structural differences have implications for a population's intrinsic viability, and by analyzing spatial composition, planners have an opportunity to evaluate how sustainable production can be achieved.

In our approach for describing spatial structure, we designated the basic building block for salmonid populations as a *branch*. In our definition, a branch component can be any reach organization containing suitable spawning habitat within a subwatershed. The quantity and interrelatedness of branches within a watershed contribute to a population's level of risk in regards to sustainable production.

Additionally, the organizational variation and quantity of branch habitat within targeted populations determine the distribution of Major (MSA) and Minor (mSA) Spawning Aggregations. A rule set (figure C-2) was developed in order to clearly define and delineate MSA and mSA structure. As with branches, it is crucial to understand the geographic composition of spawning aggregations, and their associated implications, to manage for sustainable productivity.

Moving Window Methodology

Branch development
Using GIS techniques, we developed a methodology for defining and displaying branches. We applied a *moving window* design for evaluating habitat within steelhead and chinook ESA reaches. Our moving window spatial parameters were inherited from minimum branch size definitions, which are equivalent to the amount of habitat required to sustain 50 spawners (approximately 1.25 km for spring/summer chinook, and 3.0 km for steelhead). These stream distances, then, became the calculated lengths for our moving window spatial theme.

Using linear referencing techniques, we compiled tabular descriptions for the moving window features (figure C-1). Each window was addressed with a "from", "to", and feature code attribute. The addresses were offset by 200 m increments, so that for each reach, the window began at 0 m and stopped at 3000 m (steelhead) or 1250 m (chinook), and then continued upstream at 200 m, ending at 3200m (steelhead) or 1450 m (chinook). This pattern continued until the headwaters of the hydrologic feature were reached. The

result was a set of overlapping segments representing a *moving window* spatial theme (figure C-1b).

Figure C-1. Address table for linear referencing of "moving windows."

FEATURE ID		BRANCHING PARAMETERS			
LLID	STREAM NAME	FROM CHINOOK(m)	TO CHINOOK(m)	FROM STEELHEAD(m)	TO STEELHEAD(m)
1190674487624	Pettijohn Creek	0	1250	0	3000
1190674487624	Pettijohn Creek	200	1450	200	3200
1190674487624	Pettijohn Creek	400	1650	400	3400
1190674487624	Pettijohn Creek	600	1850	600	3600
1190674487624	Pettijohn Creek	800	2050	800	3800

The second step was to identify each window's intrinsic values and calculate an average rating. The mean intrinsic calculation was our fundamental metric for determining which widows qualified for *branch* status. Because our definition stated that branches could only contain "high" or "moderate" values (and hence, the most productive habitat), it was necessary to determine the average intrinsic rating and attribute it to individual windows. We achieved this by intersecting our moving window features with those from our intrinsic

Figure C-1b. Example of spring chinook "moving window" linear referencing

potential analysis, and then summarizing the mean rating for the segments underlying each window. From this analysis, we queried for where the mean intrinsic value was at least equal to "moderate" and saved it as a new spatial theme. In this way, our moving windows are represented as a spatially derived moving average of intrinsic habitat quality.
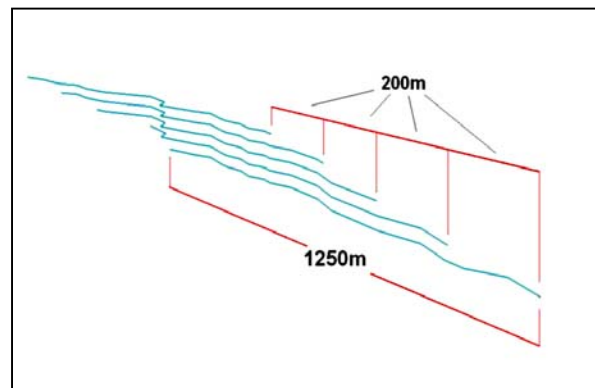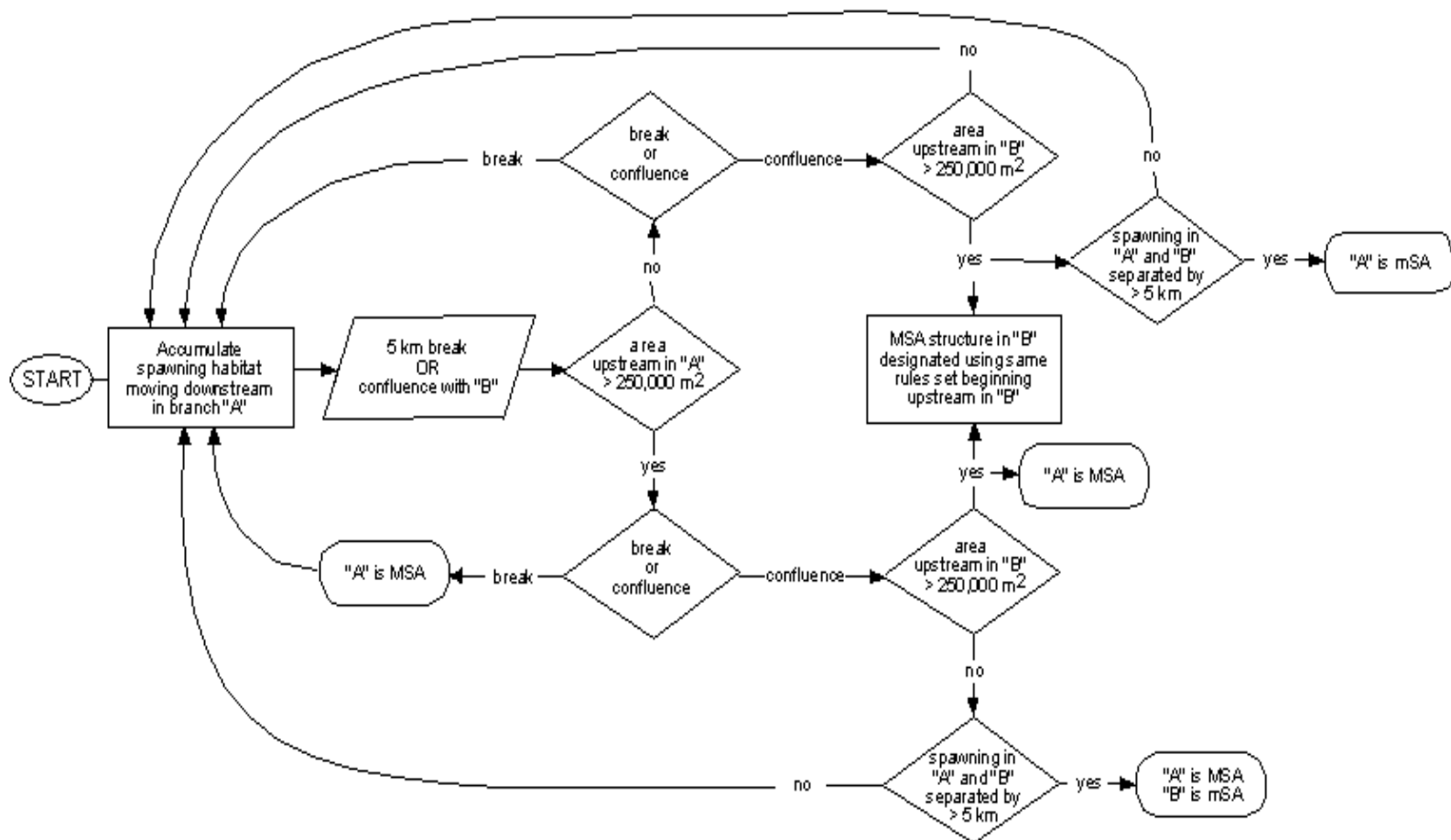
MSA development
Once our branched distribution was spatially defined, we delineated MSA and mSA subwatersheds. Major spawning aggregations were defined as a system of one or more branches that contain sufficient habitat to support 500 spawners. For spring/summer chinook, this value was 100,000m2, and for steelhead it equaled 250,000m2. We generated aggregation values by using hydrology tools within the GIS. Most commonly, these tools are utilized for calculating hydrographic features such as flow direction and accumulation, and watershed delineation.

In our evaluation, we employed flow accumulation functions (using the weighted area calculations from the intrinsic analysis) to calculate potential salmonid production. Starting from the highest elevation within a hydrologic basin, the aggregation continued

downstream, accumulating branch habitat until the watershed outlet was reached. This technique produced a hydrologically accumulated grid which was weighted by the quantity of moderate and high intrinsic habitat within our previously defined branches. Using spatial analyst, we then subtracted the topographically derived (unweighted) flow accumulation from the intrinsically weighted accumulation grid. These results were then divided by 250,000 (steelhead) or 100,000 (chinook). The values in the resulting grid illustrated where the minimum habitat criteria for MSAs were met, so that each increasing whole number identified a new potential MSA (dependent upon other criteria within the rule set). With both branches, and MSA minimums defined, the MSA rule set was applied in order to define individual MSA (or mSA) subbasins.

Figure C-2: Decision tree: defining within Population Major and Minor Spawning Areas (summer steelhead).

Figure C-3: Example of applying MSA decision flow chart to define spawning aggregations within a hypothetical population.

Stream diagram to illustrate decision making process for MSA/mSA   designation.

Arabic numbers 1-8 indicates a branch and possible start point. Higher order streams 9-14 are also labeled using arabic numerals. Each of seven confluences are marked with a black circle and labeled numerically (c1-c7). Five kilometer breaks in spawning habitat are indicated by a dash across the stream and labeled b1 and b2. Stars are the point at which the minimum potential spawning area to achieve MSA   status has been reached.
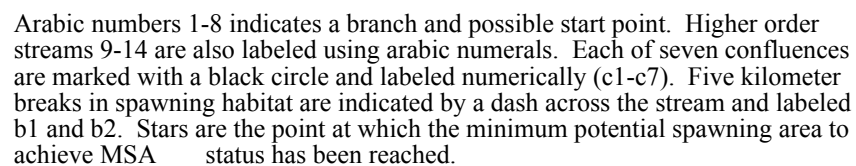
Figure C--4 *Spring Chinook **Basic size - Simple linear pattern(category A)***

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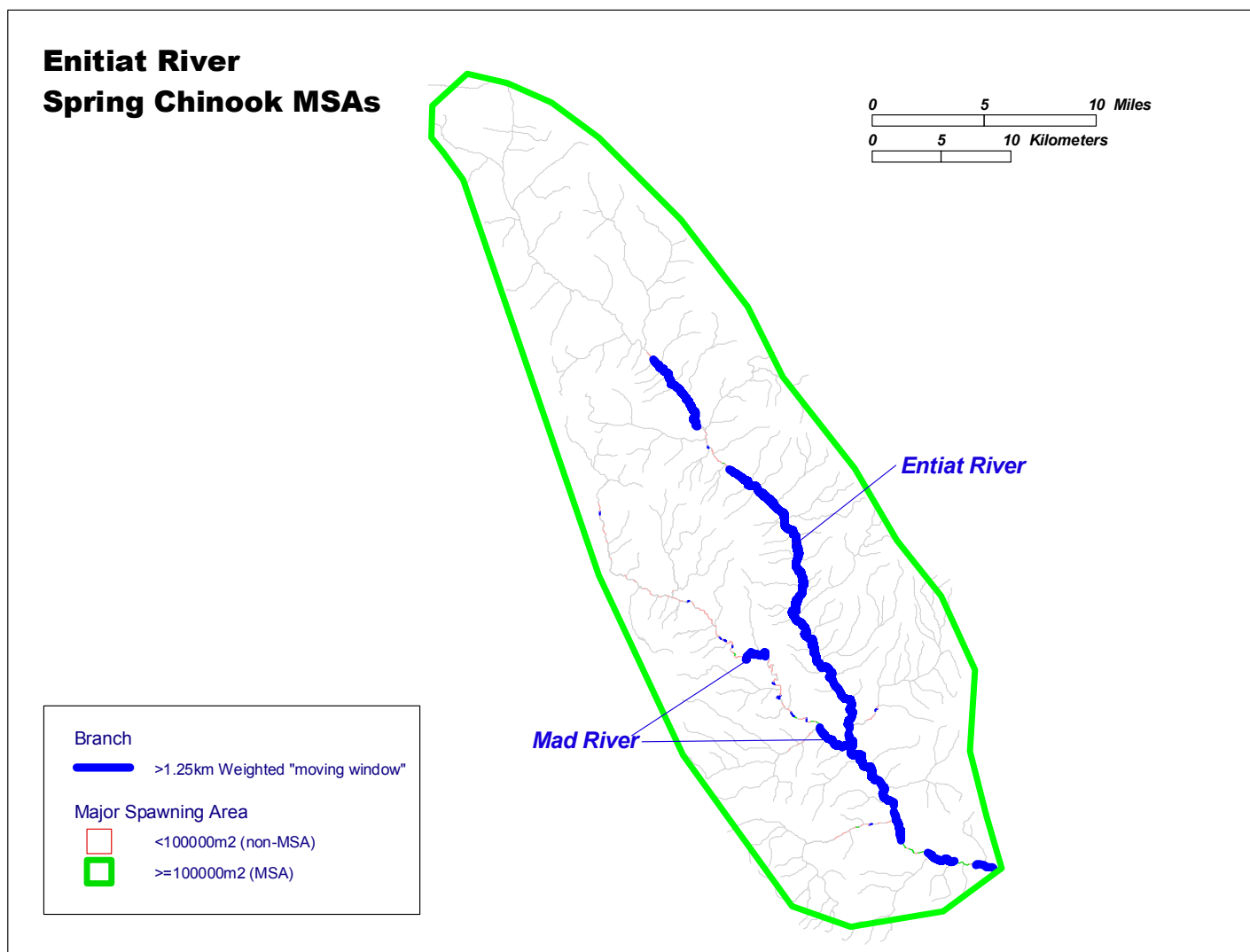
Figure C-5: *Example: Spring Chinook. Extra Large Size egory. Dendritic pattern (Category B)*

Wenatchee River
Stream Type Chinook
MSAs

NAPEEQUA R
CHIWAWA R
WHITE R
CHIKAMIN CR
LITTLE WENATCHEE R
NASON CR
WHITEPINE CR
WENATCHEE R
CHUMSTICK CR
CHIWAUKUM CR
EAGLE CR
JACK CR
ICICLE CR
WENATCHEE R
PESHASTIN CR
MISSION CR

Branch

>1.25km Weighted "moving window"

Major Spawning Area

<100000m2 (non-MSA)

>=100000m2 (MSA)

water temperature > 22C
(maximum weekly mean)

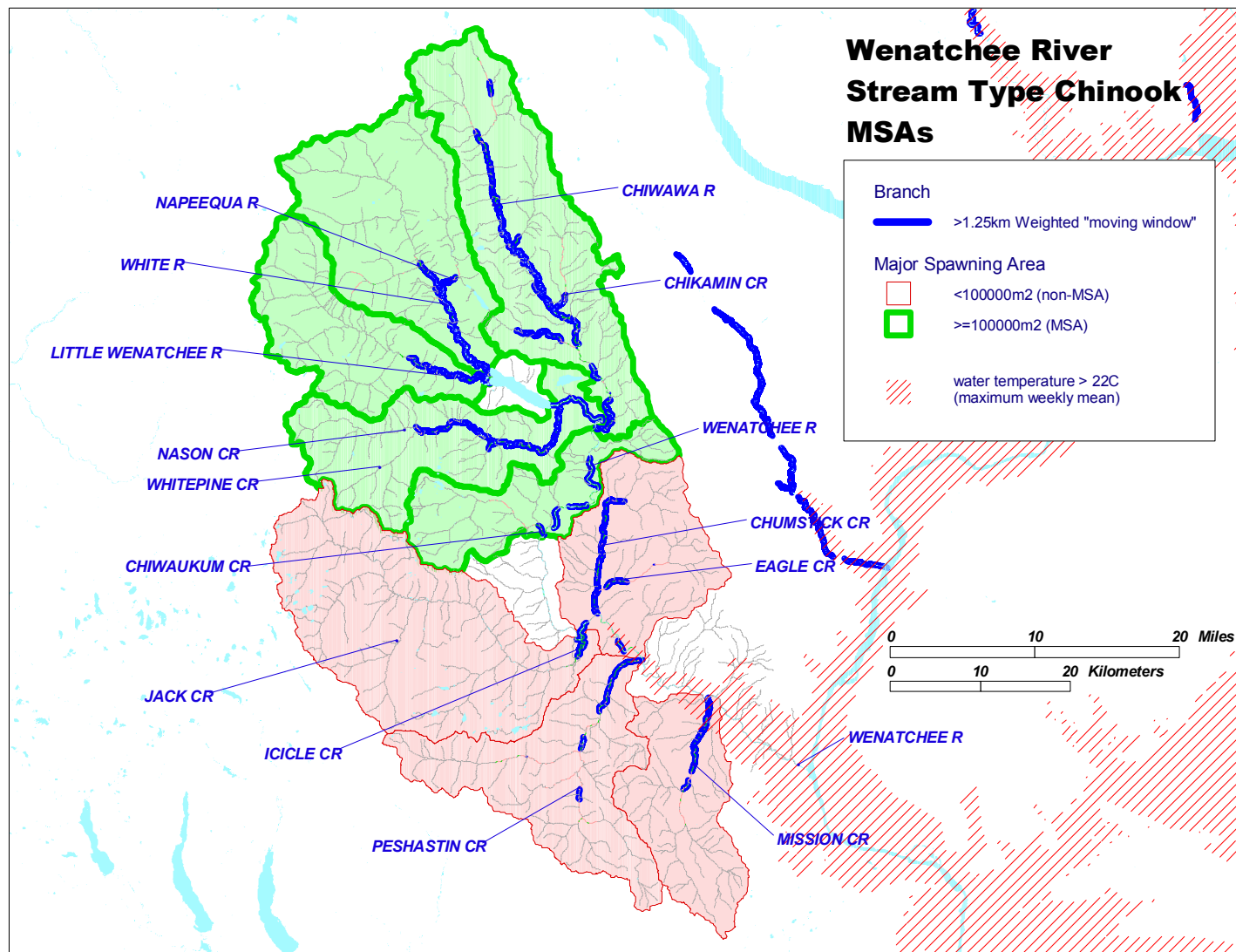0   10   20 Miles

0   10   20 Kilometers

Figure C-6: Example: Steelhead **Large Size Group - Trellis pattern (Category D)**